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CM nucleic - nucleic search, using sw model

Run on: December 14, 2005, 03:18:11 ; Search time 5462 Seconds (without alignments)

11041.908 Million cell updates/sec

Title: US-10-826-929A-1

Perfect score: 1061

Sequence: 1 agccaaaggcgggatatt.....tacagaaaaaggcaatcaga 1061

Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing First 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1061	100 0	1061	13 AF197241	AF197241 Influenza
2	1056.2	99.5	1061	13 AF197248	AY273168 Influenza
3	1053	99.2	1061	13 AF197248	AF197248 Influenza
4	1051.4	99.1	1061	13 AF197247	AF197247 Influenza
5	1048.2	98.8	1062	13 FLAHAH3B	L39914 Influenza A
6	1043.4	98.3	1060	13 EIVVY14059	Y14059 Influenza A
7	1041.8	98.2	1060	13 EIVVY14060	Y14060 Influenza A
8	1041.8	98.2	1062	13 FLAHAH3D	L39916 Influenza A
9	1039.2	97.9	1100	13 EIVVY14058	Y14058 Influenza A
10	1038.6	97.9	1062	13 FLAHAH3F	L39918 Influenza A
11	1035.4	97.6	1061	13 AF197242	AF197242 Influenza
12	1033.8	97.4	1062	6 BD244631	BD244631 Low tempe
13	1033.8	97.4	1062	6 AR254631	AR254631 Sequence
14	1033.8	97.4	1062	6 AR343239	AR343239 Sequence
15	1033.8	97.4	1062	6 AR45506	AR45506 Sequence
16	1033.8	97.4	1062	6 AR609062	AR609062 Sequence
17	1033.8	97.4	1062	13 FLAHAH3A	L39913 Influenza A
18	1032.2	97.3	1062	6 BD244629	BD244629 Low tempe

## ALIGNMENTS

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		DEFINITION	Influenza A virus (A/equine/Kentucky/1/98 (H3N8)) hemagglutinin precursor (HAL) mRNA, partial cds.				
		ACCESSION	AF197241				
		VERSION	AF197241.1	GI:6651502			
		KEYWORDS					
		SOURCE	Influenza A virus (A/equine/Kentucky/1/98 (H3N8))				
		ORGANISM	Influenza A virus (A/equine/Kentucky/1/98 (H3N8))				
		Viruses:	ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.				
		REFERENCE	1 (bases 1 to 1061)				
		AUTHORS	Lai, A.C., Chambers, T.M., Holland, R.E., Jr., Moreley, P.S., Haines, D.M., Townsend, H.G. and Barrand-deigily, M.				
		TITLE	Diverged evolution of recent equine-2 influenza viruses in the Western Hemisphere				
		JOURNAL	Arch. Virol. 146 (6), 1063-1074 (2001)				
		PUBMED	1150416				
		REFERENCE	2 (bases 1 to 1061)				
		AUTHORS	Lai, A.C.K.				
		TITLE	Direct Submission				
		JOURNAL	Submitted (21-OCT-1999) Microbiology & Molecular Genetics, Oklahoma State University, 306 Life Science East, Stillwater, OK 74078, USA				
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	DEFINITION	Influenza A virus (A/equine/Oklahoma/2000 (H3N8) ) hemagglutinin precursor (HA1) gene, partial cds.
	ACCESSION	AY273168
	VERSION	AY273168.1 GI:33415851
	KEYWORDS	Influenza A virus (A/equine/Oklahoma/2000 (H3N8) ) Influenza A virus (A/equine/Oklahoma/2000 (H3N8) ) Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A.
	SOURCE	
	ORGANISM	Lai, A.C.K., Rogers, K.M., Glaser, A., Tudor, L. and Chambers, T.
	ORGANISM	
	DEFINITION	Alternate circulation of recent equine-2 influenza viruses (H3N8)
	TITLE	from two distinct lineages in the United States
	JOURNAL	Virus Res. 100 (2), 159-164 (2004)
	PUBLISHED	15019234
	REFERENCE	2 (bases 1 to 1061)
	AUTHORS	Lai, A.C.K.
	TITLE	Direct Submission
	JOURNAL	Submitted (10-APR-2003) Microbiology & Molecular Genetics, Oklahoma State University, 306 Life Science East, Stillwater, OK 74078, USA
	FEATURES	Location/Qualifiers
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Qy	61	CCCATGGCTTACAGTCAAACCCACCACTGGAAACACAGGCCACATTATGTCGG	120	DEFINITION	Influenza A virus (A/equine/Kentucky/1/96 (H3N8)) hemagglutinin precursor (HA1) mRNA, partial cds.
Db	61	CCCATGGCTTACAGTCAAACCCACCACTGGAAACACAGGCCACATTATGTCGG	120	ACCESSION	AF197248
				VERSION	1 GI:6551516
				KEYWORDS	
				ORGANISM	Influenza A virus (A/equine/Kentucky/1/96 (H3N8)) viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzaviridae; Influenzavirinae A.
				REFERENCE	1 (bases 1 to 1061)
				AUTHORS	Lai, A.C., Chamberlain, T.M., Holland, R.E. Jr., Morley, P.S., Haines, D.M., Townsend, H.G. and Barrangou, M.
				TITLE	Diverged evolution of recent equine-2 influenza (H3N8) viruses in the Western Hemisphere
				JOURNAL	Arch. Virol. 146 (6), 1063-1074 (2001)
				PUBLMED	11504416
				REFERENCE	2 (bases 1 to 1061)
				AUTHORS	Lai, A.C.K.
				TITLE	Direct Submission
				JOURNAL	Submitted (21-Oct-1999) Microbiology & Molecular Genetics, Oklahoma State University, 306 Life Science East, Stillwater, OK 74078, USA
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				Matches	1056; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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 VERSION 1  
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 1 (bases 1 to 1762)  
 AUTHORS Daly, J. M., Lai, A. C., Binns, M. M., Chambers, T. M., Barrandeguy, M. and  
 Mumford, J. A.  
 TITLE Antigenic and genetic evolution of equine H3N8 influenza A viruses  
 J. Gen. Virol. 77 (pt 4), 661-671 (1996)  
 PUBMED 8627254  
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 QY 1021 TGGCACTGGATGGATGGAAATACCAAGAAATCAGA 1061  
 DB 1021 TGGCACTGGATGGATGGAAATCAGA 1061

RESULT 6  
 EIVY14059 EIVY14059 1060 bp RNA linear VRL 18-APR-2005  
 DEFINITION Influenza A virus (A/equi 2/Alvdalen/96 (H3N8)) gene for hemagglutinin HA1 subunit, isolate A/equi 2/Alvdalen/96.

ACCESSION Y14059  
 VERSION Y14059\_1  
 KEYWORDS hemagglutinin HA1 subunit.

SOURCE Influenza A virus (A/equi 2/Alvdalen/96 (H3N8))  
 ORGANISM Influenza A virus (A/equi 2/Alvdalen/96 (H3N8))  
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

REFERENCE Influenza virus A.  
 AUTHORS Oxburgh, L., Akerblom, L., Fridberger, T., Klingeborn, B. and Linne, T.  
 TITLE Identification of two antigenically and genetically distinct  
 lineages of H3N8 equine influenza virus in Sweden  
 Unpublished

2 (bases 1 to 1060)  
 AUTHORS Oxburgh, L.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology,  
 Swedish University of Agricultural Sciences, Biomedical Centre Box  
 585, S-751 23 Uppsala, SWEDEN  
 FEATURES Location/Qualifiers  
 source /organism="Influenza A virus (A/equi 2/Alvdalen/96 (H3N8))"  
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/mol\_type="genomic RNA"  
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CDS /codon\_start=1  
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 Best Local Similarity 99.4%; Pred. No. 1.8e-21; 6; Indels 0; Gaps 0;  
 Matches 1047; Conservative 0; Mismatches 6;  
 Matches 1047; Conservative 0; Mismatches 6;  
 QY 9 CAGGGATATTCTGCAATCATGAGAACACCAATTCTGATACTGACCCATGG 68  
 DB 1 CAGGGATATTCTGCAATCATGAGAACACCAATTCTGATACTGACCCATGG 60  
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 DB 61 GTCATCACTCAAAACCCACCACTGGAAATGAGATCATTATGTCGGACACCAT 120  
 QY 129 GCGATGAAATGGAAATGGTAAACAAATACTGATGACCAATTGGGTGACAAT 188  
 DB 121 GCGATGAAATGGAAATGGTAAACAAATACTGACCAATTGGTACAAT 180  
 QY 189 GCTACTGAAATTCTGACGATTCTAGACGATTTCATGGCAAAATATGCAAACTTAAAGCTT 248  
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Qy	1029	GGGTGAGGAATATCCAGAAAGCAATCAGA 1061		Db	121	GCGTAGCAATGGAACTTGGTAAACAACTATGACCAATTGGTACAAAT	180
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				Qy	249	CTAGATGGAAAGAAATTGCACTTAAATGTCATGCTAGGAGACCCCACTTGATGTC	308
				Db	241	CTAGATGGAAAGAAATTGCACTTAAATGTCATGCTAGGAGACCCCACTTGATGTC	300
				Qy	309	TTCCAGATGAGATTGGACCTTCTATAGAAGAAGGGCTTCAGCAATTGCTAC	368
				Db	301	TTCCAGATGAGATTGGACCTTCTATAGAAGAAGGGCTTCAGCAATTGCTAC	360
				Qy	369	CCATATGACATCCCTGACTATGCTATGCTCCATTGACATGGCTAC	428
				Db	361	CCATATGACATCCCTGACTATGCTATGCTCCATTGACATGGCTAC	420
				Qy	429	GAATTCAACGCAAGGGATTCACTGGACAGGGTCACTAAACGGGAAACTGGAGCC	488
				Db	421	GAATTCAACGCAAGGGATTCACTGGACAGGGTCACTAAACGGGAAACTGGAGCC	480
				Qy	489	TGCCAAAGGGGATCACTGGGATGCCATAGTTCTAGGCGACTAACAAATTCTGGA	548
				Db	481	TGCCAAAGGGGATCACTGGGATGCCATAGTTCTAGGCGACTAACAAATTCTGGA	540
				Qy	549	AACTCTAACCCACATTGATGACATGCTTAACTAAATTCTCACAACTATAC	608
				Db	541	AACTCTAACCCACATTGATGACATGCTTAACTAAATTCTCACAACTATAC	600
				Qy	609	ATCTGGGGATTCTCACCCGAGCTAACCAACGAGACAGATTGTACATCCAAAGA	668
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				Qy	669	TCAAGCAGGTAACAGTCACAAACGATAGTCCTAAATATCGGA	728
				Db	661	TCAAGCAGGTAACAGTCACAAACGATAGTCCTAAATATCGGA	720
				Qy	729	TCTGACCCGGTTAGGGTCAATTGCACTGGGTCTATCAGGAGGTAACTGTAAA	788
				Db	721	TCTGACCCGGTTAGGGTCTATCAGGAGGTAACTGTAAA	780
				Qy	789	CCGGAGATACTCTTAATGATAAAACAGTAAAGCTCTGAACTAGTGGCACTT	848
				Db	781	CCGGAGATACTCTTAATGATAAAACAGTAAAGCTCTGAACTAGTGGCACTT	840
				Qy	849	AAATGAAAACAGGAAAGCTCTGTAATGACATGACATGACATTGTGCG	908
				Db	841	AAATGAAAACAGGAAAGCTCTGTAATGACATGACATGACATTGTGCG	900
				Qy	909	TCTGAATGATTACACCAATTGAAAGCATCCAAACGAAACATTCAAATGTGAAC	968
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				Qy	969	AAAGTTACATATGGAAAATACCAAGATACTGGGAAACACTTTAAAGCTGCCACT	1028
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				Qy	1029	GGGTGAGGAATATACCAAGAAACAACTTCATCGA	1061
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				Qy	9	CAGGGATATTCTGTCAATCATGAAAGACACCAATTGTTGATACTACTGACCAATTGG	68
				ORIGIN		RESULT 8	
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				Best Local Similarity	99.3%	Score 1041.8; DB 13; Length 1060;	
				Matches 1046; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			

LOCUS	FLAH3D	1762 bp 8s-RNA	linear	VRL 01-NOV-2004
DEFINITION	Influenza A virus (A/equine/Florida/1/93 (H3N8)) hemagglutinin precursor (HA) gene, complete cds.			
ACCESSION	L39916			240
VERSION	1			
KEYWORDS	GI:722407			
SOURCE	Influenza A virus (A/equine/Florida/1/93 (H3N8))			
ORGANISM	Influenza A virus (A/equine/Florida/1/93 (H3N8))			
REFERENCE	Influenza A viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.			300
AUTHORS	Daly, J. M., Lai, A. C., Binns, M. M., Chambers, T. M., Barrandeguy, M. and Mumford, J. A.			360
TITLE	Antigenic and genetic evolution of equine H3N8 influenza A viruses			420
JOURNAL	J. Gen. Virol. 77 (pt 4), 661-671 (1996)			420
PUBLISHED	8627254			
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Matches 1049; Conservative	0;			
Db				
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Db	1 AGCAAAAGCAAGGGGATATTCTGTCAATCATGAGAACCAATTGTACTG	60	ETVY14058	1100 bp RNA linear
Qy	61 CCCATTGGCTCTAGCTAAACCCAAACCAAGTGGAAACAAACAGCCACATTATGTCTG	120	LOCUS	VRL 18-APR-2005
Db	61 CCCATTGGCTCTAGCTAAACCCAAACCAAGTGGAAACAAACAGCCACATTATGTCTG	120	DEFINITION	Influenza A virus (A/equi 2/Soderala/94 (H3N8)) gene for hemagglutinin HAI subunit, isolate A/equi 2/Soderala/94.
Qy	121 GACACCATGAGTACCAATGGAACATCTGTAACAAACATAACTGTGACCAATTGG	180	ACCESSION	Y14058
Db	121 GACACCATGAGTACCAATGGAACATCTGTAACAAACATAACTGTGACCAATTGG	180	KEYWORDS	GI:2767369
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			ORGANISM	Virus; ssRNA negative-strand viruses; Orthomyxoviridae;
			REFERENCE	Influenzavirus A.
			AUTHORS	Oxburgh, L., Akers, L., Klingeborn, B. and Linne, T.

TITLE	Identification of two antigenically and genetically distinct lineages of H3N8 equine influenza virus in Sweden
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1100)
AUTHORS	Oxburgh, L.H.
TITLE	Direct Submission
JOURNAL	Submitted (25-JUN-1997) Oxburgh L.H., Veterinary Microbiology, Swedish University of Agricultural Sciences, Biomedical Centre Box 585, S-751 23 Uppsala, SWEDEN
FEATURES	
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exon	<p>30...&gt;1100</p> <p>/number=1</p> <p>30...&gt;75</p>
sig_peptide	
ORIGIN	
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Best Local Similarity	98.8%; Pred. No. 1.7e-230;
Matches 1047; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
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Db	2 GCAAAGCAGGGATATTCTGTCATCAGAAGACACCATATTGATACTGAT 61
Qy	62 CCATGGCTCATGTCAAACCAACAGTGGAAACAAACAGGCAACATTGCTGG 121
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Qy	302 TGATGCTTCCAGTATGAGATTGGCACTTCTGATAGAAGAAGCAGGCCCTTCAGCA 361
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Qy	362 TTGCTTACCCATATGACATCCCTGACTATGATGCTCCATTGAGCATCTCTAGG 421
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sig_peptide	30. . 74 /gene="HA" /note="putative" 75. . 1061 /gene="HA"	Db	721 ATATGGATCTCTAGGTTAGCTGGGTCAATCTAGGAGATAAGGATATCTGGACCA 780 Qy 721 ATATGGATCTCTAGGTTAGCTGGGTCAATCTAGGAGATAAGGATATCTGGACCA 780
mat_peptide	30. . 74 /gene="HA" /note="putative" 75. . 1061 /gene="HA"	Db	781 TGTAAAACCTGGATACTCTTAATGATAAACTGAACTTACTGGACCGGG 840 Qy 781 TGTAAAACCTGGATACTCTTAATGATAAACTGAACTTACTGGACCGGG 840
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ORIGIN	Query Match 97.9%; Score 1038.6; DB 13; Length 1762; Best Local Similarity 98.7%; Pred. No. 2..le-230; Matches 1041; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	Db	901 TTGTTGTTCTGATGATTACACAATGGAGCACCCACAGAAACCATTTCAA 960 Qy 901 TTGTTGTTCTGATGATTACACAATGGAGCACCCACAGAAACCATTTCAA 960
		Db	901 TTGTTGTTCTGATGATTACACAATGGAGCACCCACAGAAACCATTTCAA 960
		Db	961 ATGTGAACAAAGTTACATATGGAAATTCGCCAGTATATCAGGAAACACTTAAGC 1020 Qy 961 ATGTGAACAAAGTTACATATGGAAATTCGCCAGTATATCAGGAAACACTTAAGC 1020
		Db	961 ATGTGAACAAAGTTACATATGGAAATTCGCCAGTATATCAGGAAACACTTAAGC 1020
		Qy	1021 TGCCCACTTGGGTAGGGATAATACAGAAAAGGAAATCTAGA 1061
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		Qy	RESULT 1.1
		Db	AFL197242 LOCUS AF197242 Influenza A virus (A/equine/Florida/1/94 (H3N8) ) hemagglutinin DEFINITION precursor (HAL) mRNA, partial cds.
		Db	ACCESSION AF197242 VERSION AF197242.1 GI: 6651504 KEYWORDS Influenza A virus (A/equine/Florida/1/94 (H3N8) ) ORGANISM Influenza A virus (A/equine/Florida/1/94 (H3N8) ) Viruses: ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A; 1. (bases 1 to 1061)
		Qy	REFERENCE Lai A.C., Chambers T.M., Holland, R.E. Jr., Morley, P.S., Haines D.M., Townsend, H.G. and Barrandeguy, M. TITLE Diverged evolution of recent equine-2 influenza (H3N8) viruses in the Western Hemisphere JOURNAL Arch. Virol. 146 (6), 1063-1074 (2001) PUBLMED 11504416 FEATURES 2. (bases 1 to 1061) AUTHORS Lai A.C.K. TITLE Direct Submission JOURNAL Submitted (21-Oct-1999) Microbiology & Molecular Genetics, Oklahoma State University, 306 Life Science East, Stillwater, OK 74078, USA FEATURES Source 1. .organism="Influenza A virus /A/equine/Florida/1/94 (H3N8) " /virion /mol_type="mRNA" /isolate="A/equine/Florida/1/94" /noTaxon="H3N8" /db_xref="taxon:217815" 1. .1061 /Gene="HAL" 30. >1061 /Gene="HAL" /codon_start=1 /product="hemagglutinin precursor" /protein_id="AAP2346.1" /db_xref="GI: 6651505" /translaton="MKTTIILILTHWAYSONPTSGNNTATCLGHHAVANGTLVKI"
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Query Match						
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Matches 1045;	98.5%;	Pred. No.	1..e-229;	Indels	0;	
Conservative 0;	Mismatches 16;	Gaps	0;			
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Db	1 AGCAAAAGCAGGGGATATTCTGTCATGAGAGACCAATTGATGACTACTGA	60				
Qy	61 CCCATGGGTCTAGCTACGTCAAAACCCACCGTGGAAACACAGGCCACATATTGATGCTGG	120				
Db	61 CCCATGGGTCTAGCTACGTCAAAACCCACCGTGGAAACACAGGCCACATATTGATGCTGG	120				
Qy	121 GACCATGCGATGCAATGGACATGGTAAACATACTGATGACCAAATGAGG	180				
Db	121 GACCATGCGATGCAATGGACATGGTAAACATACTGATGACCAAATGAGG	180				
Qy	181 TGACAAATGCTACTGAAATTAGTTCAGGATTTCAATAGGGAAAATATGCCAACATCTCAT	240				
Db	181 TGACAAATGCTACTGAAATTAGTTCAGGATTTCAATAGGGAAAATATGCCAACATCTCAT	240				
Qy	241 ATAAAATGCTAGATGGAAATAATGCACTTAAATAGATGCAATGCTAGGAGCCCCACT	300				
Db	241 ATAGATGTTAGATGGAAATAATGCACTTAAATAGATGCAATGCTAGGAGCCCCACT	300				
Qy	301 GTGATGCTTCAGTATGAGAAATTGGGACTCTCATGAAAGAAGGAGCGCTTTAGCGA	360				
Db	301 GTGATGCTTCAGTATGAGAAATTGGGACTCTCATGAAAGAAGGAGCGCTTTAGCGA	360				
Qy	361 ATGGTACCCATATGACATCCCTGATATGCACTGGTCTCGTCATTTAGATCTCTCG	420				
Db	361 ATGGTACCCATATGACATCCCTGATATGCACTGGTCTCGTCATTTAGATCTCTCG	420				
Qy	421 GAACTTAAAGAATTCAACGAGGGATTCACTGGACAGGGATTCACTGGACAAACGGAA	480				
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Qy	481 GTGGAGCTGCAAAAGGGATCATGCCGATAGTTCTTAGCCGACTGAAATTGGCTAACAA	540				
Db	481 GTGGAGCTGCAAAAGGGATCATGCCGATAGTTCTTAGCCGACTGAAATTGGCTAACAA	540				
Qy	541 AATCTGGAAACTTAACTCCACATTTGAATGTCATCTGAACTTAAATTGGCTAACAA	600				
Db	541 AATCTGGAAACTTAACTCCACATTTGAATGTCATCTGAACTTAAATTGGCTAACAA	600				
Qy	601 AACTATACTCTGGGATTCACTCCACATTTGAATGTCATCTGAACTTAAATTGGCTAACAA	660				
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Qy	661 TCCAGAATCAGGAGCTAACGTTCAACAAAAGGTCACAAACAGGATAGTCTCTTA	720				
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Db	721 ATATGGATCTAGACCTGGGGTTAGGGCTAACATGGCAGGATAAGCATACTGGACCA	780				
Qy	781 TTGTAACACTCTGGAGATACTCTTAATGATAACAGTAACTGAACTGACCGGG	840				
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Qy	841	GATATTAAATGAAAAAGGGAAAGCTCTGTATGAGATCAGATGCCATAGACA	900
Db	901	TCTGTGTCTGATGATGTTACACCAATGGAAACATCCCCAACGACAAACCAATTCTCAA	960
Qy	901	TCTGTGTCTGATGATGTTACACCAATGGAAACATCCCCAACGACAAACCAATTCTCAA	960
Db	961	ATCTGAGAAACTTACATATGGAAAATGCCCAAGTATATCAGGCCAACACTTAAAGC	1024
Qy	961	ATCTGAGAAACTTACATATGGAAAATGCCCAAGTATATCAGGCCAACACTTAAAGC	1024
Db	1021	TGCCCACTGGATACCGAGATACCGAGAAAGCTATCAGA 1061	
Qy	1021	TGCCCACTGGATACCGAGAAAGCTATCAGA 1061	
Db	1021	TGCCCACTGGATACCGAGAAAGCTATCAGA 1061	
<b>RESULT 12</b>			
	BD244631	BD244631	1762 bp
	LOCUS	BD244631	DNA
	DEFINITION	Low temperature-adaptable equine influenza virus.	linear
	ACCESSION	BD244631	
	VERSION	BD244631.1	GI:33 054401
	KEYWORDS	JP 2002522078-A/7.	
	SOURCE	Equine influenza virus H3N8	
	ORGANISM	Equine influenza virus H3N8	
	Viruses	ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.	
	REFERENCE	1 (bases 1 to 1762)	
	AUTHORS	Dowing, P.W. and Youngner, J.S.	
	TITLE	Low temperature-adaptable equine influenza virus	
	JOURNAL	Patent: JP 2002522078-A 23-JUL-2002; THE UNIVERSITY OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION	
	COMMENT	OS Equine influenza virus H3N8	
	PN	JP 2002522078-A/7	
	PD	23-JUL-2002	
	PP	12-AUG-1999 JP 20000565137	
	PR	13-AUG-1998 US 09/113321	
	PI	PATRICIA W DOWLING, JULIUS S YOUNGNER	
	PC	C12N15/09 A61K39/145, A61P31/16, C07K14/11, C12N7/04, C12R1/92,	
	PC	C12N15/00	
	CC	Low temperature-adaptable equine influenza virus FH	key
	Location/Qualifiers		
	CDS	(30) . (1724) .	
	Location/Qualifiers		
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	ORIGIN		
	FEATURES		
	source	97.4% ; Score 1033.8 ; DB 6 ; Length 1762;	
	Best Local Similarity	98.4% ; Pred. No. 2.7e-229;	
	Matches 1044 ; Conservative	0 ; Mismatches 17 ; Indels 0 ; Gaps 0 ;	
Qy	1	AGCAAAAGCAGGGATATTCTCTGTCACTCATGAAAGAACCAATTCTGATACTCTGA	60
Db	1	AGCAAAAGCAGGGATATTCTCTGTCACTCATGAAAGAACCAATTCTGATACTCTGA	60
Qy	61	CCCATGGTCTAGTCAAACCCACCGTGAACACAGCCACATTATGTCCTGG	120
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Qy	121	GACACATGCACTGAAATGGAAACATTGTAAAAACATAACTGATGCCAAATGTGAGC	180
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Qy	181	TGACAAATGCACTGAAATGGAAACATTGTAAAAACATAACTGATGCCAAATGTGAGC	240
Db	181	TGACAAATGCACTGAAATGGAAACATTGTAAAAACATAACTGATGCCAAATGTGAGC	240

		FEATURES	source	Location/Qualifiers
Qy	241	ATAAAGTCTAGATGGAAATAATGCCAATTAAATAGATGCCAATGCTAGAGACCCCACT	300	1. -1762
Db	241	ATAGATGCTCTAGATGGAAATAATGCCAATTAAATAGATGCCAATGCTAGAGACCCCACT	300	/organism="unknown" /mol_type="genomic DNA"
Qy	301	GTGATGTCCTCCAGATAGAAATTGGAACTCTTCATAGAAAGGAGCGGTTTCAAGCA	360	ORIGIN
Db	301	GTGATGTCCTTCAGATGGAAATTGGAACTCTTCATAGAAAGGAGCGGTTTCAAGCA	360	Query Match 97.4%; Score 1033.8; DB 6; Length 1762;
Qy	361	ATTGGTACCCATATGACATCCCTCGGTCCATTGGCTCTCATAGAAAGGAGCGGTTTCAAGCA	420	Best Local Similarity 98.4%; Pred. No. 2.7e-229; Mismatches 0; Indels 0; Gaps 0;
Db	361	GTGATGTCCTTCAGATGGAAATTGGCTCTCATAGAAAGGAGCGGTTTCAAGCA	420	Matches 1044; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy	421	GAACATTAGAATTACAGAGAGGGATACATGGACGGTGTCACTAAAGGGAA	480	1 AGCAAAACGAGGGATATTCTGCAATTATGAAAGAACATTGATGACTACTGAA
Db	421	GAACATTAGAATTACAGAGAGGGATACATGGACGGTGTCACTAAAGGGAA	480	1 AGCAAAACGAGGGATATTCTGCAATTATGAAAGAACATTGATGACTACTGAA
Qy	481	AAACATTGGAAATTCAAGGAGGGATACAGGACGGTGTCACTAAAGGGAA	540	61 CCCATTGGGTCTACAGTCAAACCAAGCTGAAAAGAACAGGCCAATTGCTGG
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Qy	541	AATCTGGAAACTCTTACCCACATTGAAATGTCGAATGGCTAACTAA	600	121 GACACATGCGATGCAATGGCAATTGCAACAACTGATGACCAATTGAGG
Db	541	AATCTGGAAACTCTTACCCACATTGAAATGTCGAATGGCTAACTAA	600	61 GACACATGCGATGCAATGGCAATTGCAACAACTGATGACCAATTGAGG
Qy	601	AACATACATCTGGGGATTCAACCCAGCTACCCAGGCTAACCAACGAGCAATTGTCAC	660	121 GACACATGCGATGCAATGGCAATTGCAACAACTGATGACCAATTGAGG
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Qy	661	TCCAGAATCTGGGATTAACGCTCTAACAAAGGAGTCAACAAACGATAGTCCTTA	720	181 TGCAAAATGCTACTGAAATTAGTCAGGCAATTTCAGGAAATATGCAAACTCAT
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Db	721	ACATGGGATCTAGACCTGGTCAATTGGCGGTCATACCCAGGCTAACAAAGGAA	780	241 ATAAAGTCTCTAGATGGAGAAATTGCACTTATAGATGCAATGCTAGGAGACCCACT
Qy	781	TTGTAACACTGGAGATATCTTAATGATAAACAGTAATGCCAACTTAGTTGCCACCGGG	840	301 GTATGTCTTCAGATAGAAATTGGACACTTCTCATAGAAACAGCGGCTTTCAGCA
Db	781	TTGTAACACTGGAGATATCTTAATGATAAACAGTAATGCCAACTTAGTTGCCACCGGG	840	301 GTATGTCTTCAGATAGAAATTGGACACTTCTCATAGAAACAGCGGCTTTCAGCA
Qy	841	GATATTAAATTGAAAAGGGAAAAGCTCTGTAATGAGATAGATGCCAACTTAGTTGCCACCGGG	900	361 ATTCCTCCCATATGACATCCCTGACTATGCACTGCTCGGTCAATGCTAG
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Qy	901	TTTGTGTTGTTGTTGAAATTACACCAATTGAAACCATTTCAA	960	421 GAACATTAGAACTTACACCGGATTCACTGGGATCTTCATAGAAGGAGAA
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Qy	1021	TGGCACTGGATAGGAATATCCAGAAAGCAATTGAGA	1061	601 AACATACATCTGGGGATTCAACCCAGGCTAACAAAGGAGTCAAAACGAAATTGTCAC
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LOCUS		Sequence	10 from patent US 6482414.	780
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ACCESSION		AR254631.1	GI:27303652	780
VERSION				781 TTGAAAACCTGGGATCTCCATAGGAACTTACTGGCACTTACTGGCACTTACTGGCACTT
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SOURCE				841 GATATTAAATTGAAAAGGGAAAAGCTCTGTAATGAGATGAGCTACCCATTAGACA
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AUTHORS				841 GATATTAAATTGAAAAGGGAAAAGCTCTGTAATGAGATGAGCTACCCATTAGACA
TITLE				901 TTGTGTTGTTGTTGAAATTACACCAATTGAAAGCATCCCAACGAAACCAATTCTCAA
JOURNAL				901 TTGTGTTGTTGTTGAAATTACACCAATTGAAAGCATCCCAACGAAACCAATTCTCAA
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Qy	961	ATGGAACAAAGTTACATATGAAAATGCCCAAGTATACTTTAACGC	1020	Db	541	AATCTGGAAACTCTTACCCCATCTGACATGCTAACATAAAATTCTGACA	600
Db	961	ATGTAACAAAGTTACATATGAAAATGCCCAAGTATACTTTAACGC	1020	Qy	601	AACATACATCTGGGATTCATCCGAGCTAACACAAAGGAGTTGATA	660
Qy	1021	TGGCACTGGATGAGGAATATACAGAAAAGCAAAATCAGA	1061	Db	601	AACATACATCTGGGATTCATCCGAGCTAACACAAAGGAGTTGATA	660
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LOCUS	AR343239	AR343239	AR343239	AR343239	AR343239	AR343239	AR343239
DEFINITION	Sequence 10 from patent US 6579528.	1762 bp	DNA	linear	PAT 17-AUG-2003		
ACCESSION	AR343239						
VERSION	GI:33738757						
KEYWORDS	Unknown.						
SOURCE	ORGANISM	Unclassified.					
REFERENCE	1. (bases 1 to 1762)						
AUTHORS	Dowling, P.W. and Youngner, J.S.						
TITLE	Cold-adapted equine influenza viruses						
JOURNAL	Patent: US 6579528-A 10 17-JUN-2003;						
FEATURES	The University of Pittsburgh - of the Commonwealth System of Higher Education; Pittsburgh, PA						
source	Location/Qualifiers						
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ORIGIN							
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Matches 1044; Conservative	0;	Mismatches 17;	Indels 0;	Gaps 0;			
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Db	1	AGCAAAGCAGGGATATTCTGTCAATCTGAGACACCATTTGTACTCTGA	60	AR45506			
Qy	61	CCCATGGGTCTACGTCAAACCAACCAAGTGGAAACACAGGCCACATTATGTCTGG	120	LOCUS	AR45506	1762 bp	DNA
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Qy	121	GACACATGCACTGGAAATGGAAACATGGTAAACAAATACTGTGAACTTATGTCTGG	120	ACCESSION	AR45506		
Db	121	GACACATGCACTGGAAATGGAAACATGGTAAACAAATACTGTGAACTTATGTCTGG	120	VERSION	AR45506.1	GI:42690326	
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Db	181	TGACAATGCTACTGAAATTGTCAGGAACTTCAATGGAAATAATGCAAACTCTAT	240	REFERENCE	Dowling, P.W. and Youngner, J.S.		
Qy	241	ATAAGTCTAGTGGAAATTGCAATTAATGATGCAATGCTTAGGAGCCCCACT	300	AUTHORS	Cold-adapted equine influenza viruses		
Db	241	ATAAGTCTAGTGGAAATTGCAATTAATGATGCAATGCTTAGGAGCCCCACT	300	JOURNAL	Patent: US 6685946-A 10 03-FEB-2004;		
Qy	301	GTCATGCTTCCAGTATGAAATTGGGACCTCTCATGAAAGAACGGCGTTTCAGCA	360	FEATURES	The University of Pittsburgh - of the Commonwealth System of Higher		
Db	301	GTCATGCTTCCAGTATGAAATTGGGACCTCTCATGAAAGAACGGCGTTTCAGCA	360	source	Education; Pittsburgh, PA		
Qy	361	ATGGTACCCATATGACATCCCTGACTATGCTCGGTCATCTGATCCCTAG	420	LOCATION/Qualifiers	Location/Qualifiers		
Db	361	ATGGTACCCATATGACATCCCTGACTATGCTCGGTCATCTGATCCCTAG	420	ORIGIN	1.1762		
Qy	421	GAACATGAAATTCAACAGGAGGATTCACATGGACAGGTGTCACCTAACAAAGGAA	480	ORGANISM	/organism="unknown"		
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Suit No.	Score	Query Match	Length	DB	ID	%	Query Match	Length	DB	ID	Description
1	1061	100.0	1061	14	ADW87317						Adw87317 Equine-2
2	1033.8	97.4	1762	3	AAZ50976						Aaz50976 Cold-adap
3	1032.2	97.3	1762	3	AAZ50975						Aaz50975 Wild type
4	1019.2	96.1	1698	2	AAZ30213						Aaz30213 Sequence
5	1018.4	96.0	1762	2	AAQ29112						Aaq29112 BIV HA (A
6	987.4	93.1	1788	1	AAU71067						Aau71067 Sequence
7	987.4	93.1	1797	2	AAQ04597						Aaq04597 Equine he
8	984	92.7	1698	3	AAZ30211						Aaz30211 Sequence
9	984	92.7	1698	3	AAZ47007						Aaz47007 Equine in
10	976.2	92.0	1762	2	AAQ29111						Aaq29111 BIV HA (A
11	947.2	89.3	1698	2	AAV49391						Aav49391 BIV Fonda
12	607.2	57.2	1777	2	AAQ72855						Aaq72855 Full- leng
13	601.6	56.7	1765	6	ABA93937						Aba93937 Influenza
14	598.4	56.4	1764	6	ABA93944						Aba93944 Influenza
15	595.6	54.2	1762	1	AAU70642						Aau70642 Sequence
16	579.2	54.6	1762	14	ADY27335						Ady27335 Hemaggliuc
17	574.4	54.1	1762	14	ADY27539						Ady27539 Hemaggliuc
18	569.8	53.7	1755	2	ADY27533						Ady27533 Hemaggliuc
19	568	53.5	1762	14	ADY27541						Ady27541 Hemaggliuc

20	566..4	53..4	1762	14	ADY27537	Hemagglut
21	566..2	53..4	1091	6	ABQ82724	Influenza
22	566..8	53..2	1745	14	ADY7531	Ady7531
23	558..2	52..6	1653	6	ABQ82723	Influenza
24	556..2	52..4	987	6	ABQ82726	Influenza
25	554..4	52..3	987	6	ABQ82725	Influenza
26	549..2	51..8	1793	2	AAT59212	Influenza
27	549..2	51..8	1793	2	AAX00773	Influenza
28	549..2	51..8	1793	5	AAD09586	Influenza
29	546..4	51..5	988	12	ADOL5237	Influenza
30	544..4	51..3	1757	2	AAT59216	Influenza
31	544..4	51..3	1757	2	AAX00777	Influenza
32	544..4	51..3	1757	5	AAD09590	Influenza
33	541..2	51..0	1701	2	AAY49298	SIV strai
34	541..2	51..0	1757	2	AAT5919	Influenza
35	541..2	51..0	1757	2	AAX00780	Influenza
36	541..2	51..0	1757	5	AAD09593	Influenza
37	150..4	14..2	1809	1	AAT71066	Sequence
38	150..4	14..2	1809	5	Aaq04596	Equine he
39	148..2	14..0	1759	2	AAQ29110	BIV HA (A
40	133..4	12..6	2005	3	Aaa75002	Nucleotid
41	133..4	12..6	4610	3	Aaa75005	Nucleotid
42	133..4	12..6	4930	3	Aaa75000	Nucleotid
43	127..2	12..0	1721	2	ADR29821	Adn29821
44	127..2	12..0	1721	2	AAV26247	Genomic D
	125..2	11..8	1711	6	AAL50113	Recombina
ALIGNMENTS						
RESULT 1						
ADW87317						
	ID	ADW87317	standard	DNA	1061	BP.
	XX					
	AC	ADW87317;				
	XX					
	DT	21-APR-2005	(first entry)			
	XX					
	DS	Equine-2 influenza virus hemagglutinin protein HA1 coding sequence.				
	XX					
	KW	immunostimulant; vaccine; immunization; hemagglutinin; gene; ds.				
	XX					
	OS	Influenza virus.				
	XX					
	Key	Location/Qualifiers				
	PH	30..1061				
	CDS	/*tag=	b			
		/product=	"hemagglutinin"			
		/note=	"no stop codon Given"			
		/transl_except=	(pos:369..377 aa:ProAsp)			
		/note=	"a one codon insertion alters the reading frame"			
		30..74				
		/*tag=	a			
		mat_peptide				
		/*tag=	c			
		75..1061				
		/*tag=				
		US2005032732-A1.				
	XX					
	PD	10-FEB-2005.				
	XX					
	PF	16-APR-2004;	2004US-0082629.			
	XX					
	PR	15-MAY-2003;	2003US-0470843P.			
	XX					
	PA	(LAIA/)	LAI A.			
	XX					
	PI	Lai A;				
	XX					
	WPI	2005-151686/16.				
	XX					
	DR	P-PSDB; ADW87316.				
	DR	GENBANK; AF197241.				
	XX					



Qy	961	ATCTGAACTAAAGTTACATATGAAAATGCCCCAAGTATCAGGAAACACTTTAACGC 1020	
Db	961	ATCTGAACTAAAGTTACATATGAAAATGCCCCAAGTATCAGGAAACACTTTAACGC 1020	
Qy	1021	TGGCCACTGGATGAGGAATATCAGGAAACCAAAATCAGA 1061	
Db	1021	TGGCCACTGGATGAGGAATACCGAGAAAGCAAATCAGA 1061	
RESULT 3			
	Aa250975	standard; DNA; 1762 BP.	
	XX		
	AC		
	AA250975;		
	XX		
	DT		
	XX	05-JUN-2000 (first entry)	
	DE	Wild type equine influenza virus H3N8 haemagglutinin protein DNA.	
	XX		
	KW	Haemagglutinin protein; wild type HA protein; horse; cold-adaptation; reassortant virus; temperature sensitivity; dominant interference; attenuation; antiviral; vaccine; prevention; treatment; influenza A virus infection; ds.	
	KW		
	KW		
	KW		
	OS	Equine influenza virus H3N8.	
	XX		
	Key	Location/Qualifiers	
	PH		
	CD5	30 .1727	
	FT	/*tag_ a	
	FT	/product= "HA protein"	
	FT	/note= "The coding region without the stop codon is specifically claimed"	
	XX		
	PN	WO200009702-A1.	
	XX		
	PD	24-FEB-2000.	
	XX		
	PF	99WO-US016583.	
	XX		
	PF	12-AUG-1999;	
	XX		
	PR	98US-00133921.	
	XX		
	PA	(UYPI-) UNIV PITTSBURGH.	
	XX		
	PI	Dowling PW, Youngner J;	
	XX		
	DR	WPI: 2000-224339/19.	
	DR	P-PSDB, AR70056.	
	XX		
	PT	New cold-adapted equine influenza viruses and reassortant viruses used as vaccines for treating influenza infections in animals, particularly horses, have a phenotype such as temperature sensitivity or dominant interference.	
	PT		
	PT		
	PT		
	XX		
	PS	Claim 8; Page 82-85; 127PP; English.	
	XX		
	CC	The patent discloses experimentally generated cold-adapted equine influenza viruses, and reassortant influenza A viruses comprising at least one genome segment of the cold-adapted virus, which confers at least one identifying phenotype selected from cold-adaptation, temperature sensitivity, dominant interference and attenuation. These viruses are used in therapeutic compositions e.g. vaccines for preventing or treating infections caused by influenza A viruses in animals, particularly horses. The present sequence is a DNA (newWHA1762) encoding wild type equine influenza virus H3N8 haemagglutinin (HA) protein denoted as PeiwtHAs65. This sequence is modified to generate cold-adapted equine influenza virus	
	CC		
	XX		
	XX	Sequence 1762 BP; 639 A; 334 C; 383 G; 406 T; 0 U; 0 Other;	
	Query Match	97.3%	Score 1032.2; DB 3; Length 1762;
	Best Local Similarity	98.3%	Pred. No. 3.9e-281;
	Matches 1043;	Conservative	Pred. No. 0; Missmatches 0; 18;
			Indels 0; Gaps 0;

QY	1	AGCRAAAGCAGGGGATAATTCTGTCAAATCATGAGAACCAACATTATTGTACTACTGA	60	RESULT 4
Db	1	AGCAAAGZAGGGGATTTCGTCAAATCATGAGAACCAACATTATTGTACTACTGA	60	AAZ30213 ID AAZ30213 standard; DNA; 1698 BP.
QY	61	CCCATGGCTCTAGTCAAACCAACCAACCTGAAACACAGCCACATTATGTCTGG	120	XX
Db	61	CCCATGGCTCTAGTCAAACCAACCAACCTGCAACAGCCACATTATGTCTGG	120	AC
QY	121	GACACCATCTAGTAGCAAATGGACATTTGTTAAAAACATACTGATGACCAATTGG	180	XX
Db	121	GACACCATCTAGTAGCAAATGGACATTTGTTAAAAACATACTGATGACCAATTGG	180	KW
QY	181	TGACAAATGCTACTGAAATTAGCAGGATTCAATGGAAAATATGCAACACTAT	240	KW
Db	181	TGACAAATGCTACTGAAATTAGCAGGATTCAATGGAAAATATGCAACACTAT	240	maleic anhydride; alkenyl derivative; animal vaccine; viral infection;
QY	241	ATAAAGTTCTAGTGGAAAGAAATTGCAACATTAACTAGTCAAACTGCTAGAGACCCCCACT	300	bacterial infection; ss.
Db	241	ATAAAGTTCTAGTGGAAAGAAATTGCAACATTAACTAGTCAAACTGCTAGAGACCCCCACT	300	XX
QY	301	GTGATGCTCTCCAGTATGAAATTGGACCTCTCATGAAAGGCGCTTTCAGCA	360	OS
Db	301	GTGATGCTCTCCAGTATGAAATTGGACCTCTCATGAAAGGCGCTTTCAGCA	360	Equine influenza virus.
QY	361	ATTGCTACCCATATGACATCCCTGACTATGCTGGTCCATTGTAGATCCTCTAG	420	XX
Db	361	TTGCTACCCATATGACATCCCTGACTATGCTGGTCCATTGTAGATCCTCTAG	420	FR2776928-A1.
QY	421	GAACATTAGAAATTCAACGGAGGGATTCACATGACAGGTGTCACTCAAAAGGAA	480	XX
Db	421	GAACATTAGAAATTCAACGGAGGGATTCACATGACAGGTGTCACTCAAAAGGAA	480	XX
QY	481	GTGAGCTCTGCAAAAGGGATCAACGGATAGCTTCTAGCCACTGATTGGCTAACAA	540	XX
Db	481	GTGAGCTCTGCAAAAGGGATCAACGGATAGCTTCTAGCCACTGATTGGCTAACAG	540	08-OCT-1999.
QY	541	AATCTGGAAACTCTTACCCACATTGAAATGTGACATGCTAACATAAAATTTCGACA	600	XX
Db	541	AATCTGGAAACTCTTACCCACATTGAAATGTGACATGCTAACATAAAATTTCGACA	600	98FR-0004409.
QY	601	AACATATACTCTGGGGATTCTACCCAGCTACCCAGCTAACACAGACAGAAATTGACA	660	XX
Db	601	AACATATACTCTGGGGATTCTACCCAGCTACCCAGCTAACACAGACAGAAATTGACA	660	03-APR-1998;
QY	661	TCCAGAATCAGGCGTAACACTCTACACAGGAAATTGGCTAACTGGCTAAAGGATA	720	XX
Db	661	TCCAGAATCAGGCGTAACACTCTACACAGGAAATTGGCTAACTGGCTAAAGGATA	720	98FR-0004409.
QY	721	ATATGGATCTAGACGGGTAACTCTACACAGGAAATTGGCTAACTGGCTAAAGGATA	780	XX
Db	721	ACATGGATCTAGACGGGTAACTCTACACAGGAAATTGGCTAACTGGCTAAAGGATA	780	XX
QY	781	TTGTAAAACCTGGGATATCTAACTGAACTACGTAATGGCAACTTGTGACCCGG	840	03-APR-1998;
Db	781	TTGTAAAACCTGGGATATCTAACTGAACTACGTAATGGCAACTTGTGACCCGG	840	DB 2;
QY	841	GATATTAAATTGAAACAGGGAAAGCTCTGTAAATGAGTCAGATGCCCATAGACA	900	Best Local Similarity 96.1%; Score 1019.2%; Pred. No. 1.8e-277;
Db	841	GATATTAAATTGAAACAGGGAAAGCTCTGTAAATGAGTCAGATGCCCATAGACA	900	Matches 1024; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY	901	TTTGTGTGTCTGTAATGTTACACAAATTGAAACATCCCAGAACACATTTCAAA	960	03-APR-1998;
Db	901	TTTGTGTGTCTGTAATGTTACACAAATTGAAACATCCCAGAACACATTTCAAA	960	03-APR-1998;
QY	961	ATGTGAAACAAAGTACATATTGAAATTGCAAAATGCCCAAGTATCAGCAAAACTTAAGC	1020	DB 2;
Db	961	ATGTGAAACAAAGTACATATTGAAATTGCAAAATGCCCAAGTATCAGCAAAACTTAAGC	1020	DB 2;
QY	1021	TGGCCACTGGGATGAGGAATATACCAAAGAACAAATTGAGAAATTGCAAAACT	1061	DB 2;
Db	1021	TGGCCACTGGGATGAGGAATATACCAAAGAACAAATTGAGAAATTGCAAAACT	1061	DB 2;
QY	270	TTATAGATGCAATGCTACGGACCCCCACTGTGATGCTTCAGATGAGAAATTGGGAC	329	DB 2;





Db 625 AACTATACATCTGGGGATCCATACCCGAGGCAACAAACATGAGCAGACAAATGTTATA 684  
 Qy 661 TCCAAGAATCAGGAGCTAACAGTCACAGTCACAAACAAAGTCACAAACAAATGCTTA 720  
 Db 685 TCCAAGAATCAGGAGCTAACAGTCACAGTCACAAACAAAGTCACAAACAAATGCTCA 744  
 Qy 721 ATATCGGATCTAGACCTGGCTTAGGGCTCAATCGCAGGATAAGCATATGACCA 780  
 Db 745 ACATCGGATCTAGACCTGGCTTAGGGCTCAATCGCAGGATAAGCATATGACCA 804  
 Qy 781 TTGTAACACTGGGATCTTAATGATAAACAGTGTGCACTTGACCGGG 840  
 Db 805 TTGTAACACTGGGATCTTAATGATAAACAGTGTGCACTTGACCGGG 864  
 Qy 841 GATATTAAATTTGAAACAGGAAAGCTCTGTAATGAGTCAGATGCCCATAGACA 900  
 Db 865 GATATTAAATTCGAAAGCTGTGAACTGACCCATAGACA 924  
 Qy 901 TTGTTGTTCTGATGTGATTACCAATGAAAGCATCCCACGAAACATTCAA 960  
 Db 925 CTGTTGTTCTGATGTGATTACCAATGAAAGCATCCCACGAAACATTCAA 984  
 Qy 961 ATGTCACAAAGTTTACATATGAAATGCCCCAAGTATATGCGCAAAACCTTAAAGC 1020  
 Db 985 ATGTCACAAAGTTTACATATGAAATGCCCCAAGTATATGAAAGCTGTGAGC 1044  
 Qy 1021 TGCCCACTGGGTATGAGGAATATACCAAGAAACCTTAAAGC 1061  
 Db 1045 TGCCCACTGGGTATGAGGAATATACCAAGAAACCTTAAAGC 1085

## RESULT 7

AAQ04597 standard; DNA; 1797 BP.  
 AAQ04597;  
 DT 25-MAR-2003 (revised)  
 DT 02-OCT-1990 (first entry)

XX Equine hemagglutinin H3 (EIV-A2).  
 XX Recombinant vaccines: equine influenza virus; haemagglutinin; H3;  
 KW neuraminidase; N8; ss.  
 XX Equine influenza virus.

FH Key Location/Qualifiers  
 CDS

FT 54 .1748  
 FT /product= "EIV-A2 haemagglutinin H3"  
 FT 102 .1182  
 FT /\*tag= \_b  
 FT /product= "N-terminal HA1 50kD portion"  
 FT 1186 .1748  
 FT /\*tag= \_c  
 FT /product= "C-terminal HA2 27kD portion"  
 XX US4920213-A.  
 XX PR 20-JUN-1985; 85US-00747020.  
 XX PD 24-APR-1990.  
 XX (BIOT-) BIOTECH RES PARTNERS LTD.  
 XX PI Dale B, Cordell B;  
 XX PR 21-JUL-1986; 86US-00888250.  
 XX PR 20-JUN-1985; 85US-00747020.  
 XX PA (BIOT-) BIOTECH RES PARTNERS LTD.  
 XX PI Dale B, Cordell B;  
 XX PR 1990-163647/21.  
 DR P-PSDB; AAR04943.  
 XX

PT Recombinant vaccines against equine influenza virus - produced using DNA  
 PT sequences encoding haemagglutinin and neuraminidase glyco-protein(s).  
 XX Disclosure: Page ?; 27pp; English.  
 XX  
 CC There are nine neuraminidase (NA) subtypes and twelve haemagglutinin (HA)  
 CC subtypes. The strain carrying H3N8 glycoproteins is designated equine  
 CC influenza virus (EIV) -A2. The cDNA sequences encoding these will be  
 CC useful in the construction of diagnostic probes for the disease and of  
 CC probes for obtaining new cDNAs of the mutated form of the virus.  
 CC Recombinant vaccines are produced. See also AAQ04596-004599. (Updated on  
 CC 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 1797 BP; 639 A; 341 C; 413 G; 404 T; 0 U; 0 Other;  
 SQ Query Match 93.1%; Score 987.4; DB 2; Length 1797;  
 SQ Best Local Similarity 95.7%; Pred. No. 1.8e-268;  
 SQ Matches 1015; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
 SQ  
 Qy 1 AGCAAAAGCAGGGATATTCTGTCATATGAAAGCAACCATATTGATACTGTA 60  
 Db 25 AGCAAAAGCAGGGATATTCTGTCATATGAAAGCAACCATATTGATACTGTA 84  
 Qy 61 CCAATGGGTCTACAGTCACAAACCCAAACAGTGGAAACACACGACCAATTCTGG 120  
 Db 85 CCAATGGGTCTACAGTCACAAACCCAAACAGTGGAAACACACGACCAACTGTCGG 144  
 Qy 121 GACACCATGGATGACCAATGGAAACATGTTAAACAACTATGACCAAAATGAGG 180  
 Db 145 GACACCATGGATGACCAATGGAAACATGTTAAACAACTATGACCAAAATGAGG 204  
 Qy 181 TGACAAATGCTACTGAAATTGAGCTTACAGGCAATTTCATAGGAAAAATATGCAACAACTCAT 240  
 Db 205 TGACAAATGCTACTGAAATTGAGCTTACAGGCAATTTCATAGGAAAAATATGCAACAACTCAT 264  
 Qy 241 ATAAAGTTCTGATGGAAAGAAATTCACATTAATAGTCGAATGCTAGGAGACCCACT 300  
 Db 265 ATAGGTTCTGATGGAAAGAAACTTCACATTAATAGTCGAATGCTAGGAGATCCCACT 324  
 Qy 301 GTGAGTCTTCAGTGAATGGACATCTCATAGAAAGAAGCAGGGCTTCAGCA 360  
 Db 325 GTGAGTCTTCAGTGAATGGACATCTCATAGAAAGAAGCAGGGCTTCAGCA 384  
 Qy 361 ATGGTACCCATAACATCCGTGACTTCATCCGTCAATTGTCAGTCATCTCGT 420  
 Db 385 ATGGTACCCATAACATCCGTGACTTCATCCGTCAATTGTCAGTCATCTCGT 444  
 Qy 421 GAAACATTAGAAATTTCAGCAGGAGGATTACATGAGCTGACTTCAGTCATCTCGT 480  
 Db 445 GAAACATTAGAAATTTCAGCAGGAGGATTACATGAGCTGACTTCAGTCATCTCGT 504  
 Qy 481 GTGGAGCTTCAGAAGGGATCACCCGATAGTTCTGCTGAAATTGGCTTACAA 540  
 Db 505 GTGGAGCTTCAGAAGGGCTCACCGATAGTTCTGCTGAAATTGGCTTACAA 564  
 Qy 541 ATATGGAAACTCTTACCCCAATTGTCAGTCATGCTAACTAAATAATTGCA 600  
 Db 565 ATATGGAAATTCTTACCCCAATTGTCAGTCATGCTAACTAAATAATTGCA 624  
 Qy 601 AACATACATCTGGGGATTTCATACCCGAGCTAACAAAGGTCAACAAAGGATACTCCCTA 720  
 Db 625 AACATACATCTGGGGATTTCATACCCGAGCTAACAAAGGTCAACAAAGGATACTCCCTA 744  
 Qy 721 ATATGGAAATTCTGACCGTGGTTAGGGCTCAATGGCGGATTAATGGCTATATGGACCA 780  
 Db 745 AACATGGGAACTGAGCTAACAGTAATGCTAACTGGCGGACCGGG 804  
 Qy 781 TTGAAAACCTGGAGATATCCTAAATGATAAACAGTAATGCTAACTGGCGG 840

Db	805	TTGTGAAACCTGGAGATATCCTAATGATAAACAGTAAATGGCAACTTAATGGACCCGGGG	864	QY	30	ATGAGAGAACCATATTGATACATCTACTGACCCATTGGCTAAGTCAGTAAACCCAAACC	89
QY	841	GATAATTTAAATTGAAAAGGAAAGCTGCTGTAATGGATGATGATGATGATGATGATGACA	900	Db	1	ATGAGAGAACCATATTGATACATCTACTGACCCATTGGCTAAGTCAGTAAACCCAAAGC	60
Db	865	GATAATTTAAATTGCAAAGGGAAAGCTGCTGTAATGGATGATGATGATGATGATGACA	924	QY	90	ACTGAAACAAACAGCCACATTAATGTTGGACACCATGAGTAAATGGAAATCATTTG	149
QY	901	TTTGTGTTGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGACA	960	Db	61	AGTGCAACAAACAGCCACATTAATGTTGGACACCATGAGTAAATGGAAATCATTTG	120
Db	925	CTTGTGTTGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGACA	984	QY	150	GTAAAACATATGATGACCAATTGGGCAAAATGCTGAAATGCTGAAATGCTGAAATGCA	209
QY	961	ATGTCACAAAGTGTACATATGGAAAATGCCCAAGTATATGCCAAACACTTTAACG	1020	Db	121	GTAAAACATATGATGACCAATTGGGCAAAATGCTGAAATGCTGAAATGCTGAAATGCA	180
Db	985	ATGTCACAAAGTGTACATATGGAAAATGCCCAAGTATGCCAAAGTATGCCAAAGTACA	1044	QY	210	ATTCAATAGGGAAAATATGCCAACTCATATAAAGTCTAGATGGAAAATGTGACA	269
QY	1021	TGGCCACTGGATGAGGAATATACCAAAAGGAAATTCAGA	1061	Db	181	ATTCAATAGGGAAAATATGCCAACTCATATAAAGTCTAGATGGAAAATGTGACA	240
Db	1045	TGGCCACTGGATGAGGAATTCAGGAAAGGAAATTCAGA	1085	QY	270	TTATAGATGCAATGCTAGGAGCACCCACTGATGATGATGAGAATGGGAC	329
RESULT 8							
AAZ30211				Db	241	TTATAGATGCAATGCTAGGAGCACCCATGATGATGAGAATGGGAC	300
ID	AAZ30211	standard; DNA; 1698 BP.		QY	330	CTCTCATAGAAAGGAGGCGTTTCAAGCAATTGCTACCATGATCCCTGACTAT	389
XX	AAZ30211;			Db	301	CTCTCATAGAAGGCGTTTCAAGCAATTGCTACCATGATCCCTGACTAT	360
AC				QY	390	GCATCGTCGGTCAATTGTCATTTGATGATCCTCAGGAACTTAAATCAAGCAGGAGGATT	449
XX				Db	361	GCATCGTCGGTCAATTGTCATTTGATGATCCTCAGGAACTTAAATCAAGCAGGAGGTT	420
DT	11-FEB-2000	(first entry)		QY	450	ACATGGACAGGCTTCACTCAAAACGGAAACTGGGCTGCAAAAGGGATCAGCCAT	509
XX				Db	421	ACATGGACAGGCTTCACTCAAAACGGAAACTGGGCTGCAAAAGGGATCAGCCAT	480
DE	Sequence of the haemagglutinin (HA) gene of EIV strain Newmarket 2/93.			QY	510	AGTTCTTGTGACTAAATCTGAAACTCTTACCCACATTGAT	569
XX	Haemagglutinin gene; EIV* strain Newmarket 2/93; DNA vaccine; horse;			Db	481	AGTTCTTGTGACTAAATCTGAAACTCTTACCCACATTGAT	540
KW	acrylic acid polymer; methacrylic acid polymer; copolymer;			QY	570	GTGACAATGCTTAACAAATAATTCCAAACATACTGTTGGGATTCATCACCG	629
KW	maleic anhydride; alkenyl derivative; animal vaccine; viral infection;			Db	541	GTGACAATGCTTAACAAATAATTCCAAACATACTGTTGGGATTCATCACCG	600
KW	bacterial infection; SS.			QY	630	AGCTCAAACCAAGGAGCAGAACTGATCCTAAAGTACGAGCAGTAACGTC	689
XX	Equine influenza virus.			Db	601	AGCTCAAACCAAGGAGCAGAACTGATCCTAAAGTACGAGCAGTAACGTC	660
OS				QY	690	ACAAAAAGAAGTCACAAACAGATACTGACCTTAATTCGGAATCTGGGTTAGGGT	749
XX				Db	661	ACAAAAAGAAGTCACAAACAGATACTGACCTTAATTCGGAATCTGGGTTAGGGT	720
PN	FR2776928-A1.			QY	750	CAATCGCCGGATTAAGGATATACTGGACCATGTAACCTGGAGATATCTATGATA	809
XX				Db	721	CAATCGCCGGATTAAGGATATACTGGACCATGTAACCTGGAGATATCTATGATA	780
PD	08-OCT-1999.			QY	810	AACGTAATGGCAACTTAGTGTGCACCGGGGATATTAAATTGAAACGGAAAGC	869
XX				Db	781	AACGTAATGGCAACTTAGTGTGCACCGGGGATATTGAAACGGAAAGC	840
PF	03-APR-1998;	98FR-00004409.		QY	870	TCTGTAATGAGATGAGCTGACCATGATGCTGATGCTGATGATGATGATGAA	929
XX				Db	841	TCTGTAATGAGATGAGCTGACCATGATGCTGATGATGATGATGAA	900
PR	03-APR-1998;	98FR-00004409.		QY	930	GGAGCAACCCACGAAACCATTTGAAATGTCACATATGGAAATGTC	989
XX				Db	901	GGAGCAACCCACGAAACCATTTGAAATGTCACATATGGAAATGTC	960
PA	(MERI) MERIAL SAS.			QY	990	CCGAGTATGAGCTGAAACACTTTAAGCTGGGATGAGGAATATACCAAA	1049
XX				Db	961	CCGAGTATGAGCTGAAACACTTTAAGCTGGGATGAGGAATGTGAGCA	1020
PT	Vaccine containing naked DNA and acrylic acid polymer or maleic anhydride copolymer, for protection against viral or bacterial diseases in animals.			QY	1050	AAGGAAATCGA	1061
XX				Db	1021	AAGGAAATCGA	1032
PS	Example 8: Fig 1: 34pp; French.						
XX	The present sequence represents the haemagglutinin gene of Equine influenza virus (EIV) strain Newmarket 2/93. The sequence was used to prepare a DNA vaccine for horses, represents a DNA vaccine that comprises naked DNA encoding an antigenic polypeptide, and at least one adjuvant that is an acrylic or methacrylic acid polymer or a copolymer of maleic anhydride with an alkenyl derivative. The vaccines are simple and easy to prepare (simply by mixing components) and they do not involve any strong interactions between DNA and other components that are likely to cause complex formation. The vaccines are used to protect animals (pigs, horses, dogs, cattle, cats or birds) against a wide variety of viral or bacterial infections.						
XX	Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;						
PS	Query Match 92.7%; Score 984; DB 2; Length 1698; Best Local Similarity 91.1%; Pred. No. 1..6e-267; Matches 1002; Conservative 0; Mismatches -30; Indels 0; Gaps 0;						

RESULT 9	Qy	330	CTCTTCATAGAAAAGAGCACCGCTTCAAGAATTGCTACCCATAAGACATCCCTGACTAT	389
AAZ47007	Db	301	CTCTTCATAGAAAAGAGCACCGCTTCAAGAATTGCTACCCATAAGACATCCCTGACTAT	360
ID	Qy	390	GCATCGCTGGTCCATTGTGACTCTCAGAACATTAGAAATTCAACGGAGGGATTCT	449
AAZ47007	Db	361	GCATCGCTGGTCCATTGTGACTCTCAGAACATTAGAAATTCAACGGAGGGTTCT	420
AC	Qy	450	ACATGGACAGGTGACTAAAGGAAAGTGSAGCTGCAAAGGGATCAGCCGAT	509
XX	Db	421	ACATGGACAGGTGACTCAAACGAGTGGCTGAAAGGGATCAGCCGAT	480
DT	Qy	510	AGTTCTTCTAGGCCACTGATTGGCTAACAAATTCTGGAAACTCTTACCCACATTGAAT	569
29-FBB-2000	Db	481	AGTTCTTCTAGGCCACTGATTGGCTAACAAATTCTGGAAATTCTGGATTTGAAATTGAT	540
(first entry)	Qy	570	GTGACATGCTTACAATAAAATTTCGACAAACTATACATCTGGGGATTCATCACCCG	629
XX	Db	541	GTGACATGCTTACAATAAAATTTCGACAAACTATACATCTGGGGATTCATCACCCG	600
DE	Qy	630	AGCTCAAACCAACGAGCAGAACATTGACATCCAGAACTATACATCTGGGGATTCATCAC	689
Equine influenza virus strain Newmarket 2/93 HA gene.	Db	601	AGCTCAAACGAGCAGAACATTGACATCCAGAACTATACATCTGGGGATTCATCAC	660
XX	Qy	690	ACAAAAGAGGTCAACAAACGATGCTCCATAATTGGATCTAACCTGGTTAGGGT	749
KW	Db	661	ACACAAAGAGTCACAAACGATGCTCCATAATTGGATCTAACCTGGTTAGGGT	720
recombinant; vaccine; viral vector; pathogen; adjuvant; methacrylic acid;	Qy	750	CAATGGGAGGATAAGGATATACTGGACCATTTAAACCTGGAGATACTCTTATGATA	809
maleic anhydride; alkene; derivative; animal; herpes virus; tetanus;	Db	721	CAATGGGAGGATAAGGATATACTGGACCATTTAAACCTGGAGATACTCTTATGATA	780
influenza virus; feline leukemia; canine distemper; ss.	Qy	810	AACGTAATGGCAACTTACTTGCAACCGGGATAATTAAATTGAAACAGGAAAGC	869
XX	Db	781	AACGTAATGGCAACTTACTTGCAACCGGGATAATTAAATTGAAACAGGAAAGC	840
PA	Qy	870	TCTCTTAATGAGATAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	929
(MERL-) Merial.	Db	841	TCTCTTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	900
XX	CC	930	GGAGCATCCCAAGGAAACATTGAAATTGACAAGTTACATATGGAAATTC	989
PD	CC	901	GGAGCATCCCAAGGAAACATTGACAATTGACAATTGACAATTGACAATTGACA	960
10-SEP-1999.	XX	990	CCCAAGTATATGAGCAAACACTTTAAAGCTGCCACTGGATGAGGATATACCGAA	1049
XX	PR	961	CCCAGTATATGAGCAAACACTTTAAAGCTGCCACTGGATGAGGATATACCGAA	1020
01-MAR-1999;	PF	1050	AAGGAAACAGA	1061
99WO-FR000453.	XX	AAQ29111	standard;	DNA; 1762 BP.
XX	XX	AAQ29111		
03-MAR-1998;	PR	1021	AAGGAAACAGA	1032
98FR-00002800.	XX			
XX	PS			
PI	PT			
Audonnet JP, Minke JM;	XX			
XX	DR			
WPI; 2000-022918/02.	XX			
XX	XX			
PT	Live recombinant vaccine comprising viral vector and polymeric adjuvant,			
XX	particularlly directed against animal herpes and influenza viruses.			
PS	Example 5; Fig 1; 41PP; French.			
XX	This sequence represents the haemagglutinin (HA) gene from the equine influenza virus strain Newmarket 2/93. The gene was amplified and the product was used to generate a live recombinant vaccine which comprises: (1) a viral vector including, and expressing in vivo, a heterologous nucleotide sequence particularly a gene from a pathogen; and (2) at least one adjuvant, i.e. a (meth)acrylic acid polymer or a copolymer of maleic anhydride and alkene derivatives. The vaccines are used particularly to protect against animal herpes or influenza viruses, but also feline leukemia, tetanus and canine distemper			
XX	Sequence 1698 BP; 619 A; 312 C; 372 G; 395 T; 0 U; 0 Other;			
SQ	Query Match 92.7%; Score 984; DB 3; Length 1698;			
	Best Local Similarity 97.1%; Pred. No. 1.6e-267;			
	Matches 1002; Conservative 0; Mismatches 30; Indels 0; Gaps 0;			
Qy	30 ATGAGAACCACTATTGTGACTCTGACCCATTGTGACTCTGACCTGGTCTACAGTCACAAACCCACC	89	RESULT 10	
Db	1 ATGAGAACCACTATTGTGACTCTGACCCATTGTGACTCTGACCTGGTCTACAGTCACAAACCCACC	60	AAQ29111	
		XX	AAQ29111;	
Qy	90 AGTGGAAACACAGCACATTGTGCTGGACACATTGCAATTGAAACATTG	149	AC	
Db	61 AGTGGCAACACAGCACATTGTGCTGGACACATTGCAATTGAAACATTG	120	XX	
		DT	25-MAR-2003 (revised)	
Qy	150 GTAAAAACATAACTGACCAATTGAGGTGCAAAATGCTACTGATTAGTTCAGAGC	209	DT	24-FEB-1993 (first entry)
Db	121 GTAAAAACATAACTGACCAATTGAGGTGCAAAATGCTACTGATTAGTTCAGAGC	180	XX	
		DE	EVY HA (A1/Fontainbeau/79).	
Qy	210 ATTGATAGTGGAAATATGCAACACTCATATAAGTCTAGATGGAAATTGCA	269	XX	Equine influenza virus; EVY; hemagglutinin; HA; A1/Fontainbeau/79;
Db	181 ATTGATAGTGGAAATATGCAACACTCATATAAGTGGTCTAGATGGAAATTGCA	240	KW	expression cassette; NYVAC; ALVAC; recombinant vector;
		XX	KW	polymerase chain reaction; PCR; vaccinia virus; H6 promoter;
Qy	270 TTAATAGTGGCAATGCTAGAGACCCCACTGATGCTTCAGTAGAATTGGCAC	329	KW	canarypox virus; Copehagen vaccine strain; virulence factor;
Db	241 TTAATAGTGGCAATGCTAGAGACCCCACTGATGCTTCAGTAGAATTGGCAC	300	XX	deletion loci; recipient loci; ss.
		OS		
		XX		
		PN		
				W09215672-A1.

XX	17-SEP-1992.	QY	481	GTGGAGCTGCAAAGGGATAGCCGATAGTTCTTCTGGAATTCGGCTAACAA
PD	09-MAR-1992;	Db	481	GTGGAGCTGCAAAGGGATAGCCGATAGTTCTTCTGGAATTCGGCTAACAA
XX	07-MAR-1991;	QY	541	AATCTGGAACTCTAACCCACATGATGTCACAACTAAATTCTGACA
PR	11-JUN-1991;	Db	541	AATCTGGAACTCTAACCCACATGATGTCACAACTAAATTCTGACA
PR	06-MAR-1992;	Db	541	AATCTGGAACTCTAACCCACATGATGTCACAACTAAATTCTGACA
XX	PA (VIROGENETICS CORP.	QY	601	AACTATACATCTGGGGATTCACTACCCGAGCTCAACCAACAGAGACAAATGTCACA
XX	PAoletti, E., Perkus ME, Taylor J, Tartaglia J, Norton EK;	Db	601	AACTATACATCTGGGGATTCACTACCCGAGCTCAACCAACAGAGACAAATGTCACA
PI	Riviere, M., De Taisne, C., Limbach KJ, Johnson GP, Pincus SE,	QY	661	TCCAAGATCACGAGGATTAACGTCACAAAGAAGTCACAAACATATTCCTA
PI	Francis, J., Getting RR;	Db	661	TCCAAGATTCAGCTGGGGATTAACGTCACAAAGAAGTCACAAACATATTCCTA
XX	DR; 1992-331718/40.	QY	721	ATATCGGATCTGAGACCTGGGGTTAGGGTCAATCGCAGGATACTGGACCA
XX	Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating	Db	721	ATATCGGATCTGAGACCTGGGGTTAGGGTCAATCGCAGGATACTGGACCA
PR	against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,	QY	781	TTGTAACACCTGGAGATCTTAATGATAAAACAGTATGGCAACTTAGTTGCAACGGGG
PR	mumps etc.	Db	781	TTGTAACACCTGGAGATCTTAATGATAAAACAGTATGGCAACTTAGTTGCAACGGGG
PS	Disclosure; Fig 24; 45pp; English.	QY	841	GATATTTAAATGAAACAGGAAAGACTCTGTAATGAGATCAGATGCAACCATAGACA
XX	The sequence given encodes the equine influenza virus (EIV) hemagglutinin	Db	841	GATATTTAAATGAAACAGGAAAGACTCTGTAATGAGATCAGATGCAACCATAGACA
CC	(HA) (AI/Fontainebleau/79). This sequence was used to generate an	QY	900	900
CC	expression cassette for the insertion of the EIV HA gene into NYVAC and	Db	900	900
CC	ALVAC recombinant vectors. The HA gene sequence was isolated from an EIV	QY	960	960
CC	cDNA library and was amplified by polymerase chain reaction. The HA gene	Db	960	960
CC	sequence was fragmented and then reconstituted aligned with the vaccinia	QY	961	961
CC	H6 promoter. NYVAC is derived from a Copenhagen vaccine strain of	Db	961	961
CC	vaccinia virus and ALVAC is derived from a canarypox virus which has been	QY	1020	1020
CC	modified by deletion of non-essential regions of the genome encoding	Db	1020	1020
CC	known or potential virulence factors. The insertion loci of both vectors	QY	1021	1021
CC	were engineered as recipient loci for the insertion of foreign genes. See	Db	1021	1021
CC	also AA035501-864. (Updated on 25-MAR-2003 to correct PN field.)	QY	1061	1061
SQ	Sequence 1762 BP; 626 A; 331 C; 395 G; 410 T; 0 U; 0 Other;	Db	1061	1061
	Query Match 92.0%; Score 976.2%; DB 2%; Length 1762;			
	Best Local Similarity 95.0%; Pred. No. 2; 7e-265;			
	Matches 1008; Conservative 0; Mismatches 53; Indels 0; Gaps 0;			
		RESULT 1.1		
		AAV49391	standard	
		AAV49391	BD.	1698
		XX	XX	
		AC	AAV49391;	
		XX	XX	
		DT	28-OCT-1998	(first entry)
		XX	XX	
		DE	EVV	Fontainebleau strain haemagglutinin gene.
		XX	XX	
		KW	Multivalent vaccine; horse; pathogen; respiratory disease; EHV; EIV;	
		KW	Clostridium tetani; Borrelia burgdorferi; equine influenza virus; BEEV;	
		KW	Eastern equine encephalomyelitis virus; equine herpesvirus; WEEV; VEEV;	
		KW	Western equine encephalomyelitis virus; digestive disease; rabies virus;	
		KW	Venezuelan equine encephalomyelitis virus; vector; primer; PCR;	
		KW	amplification; haemagglutinin; ss.	
		XX	XX	
		OS	Equine influenza virus.	
		FH	Key	
		CD5	CD5	
		PN	FR2751226-A1.	
		XX	XX	
		PD	23-JAN-1998.	
		XX	XX	
		FT	19-JUL-1996;	96FR-00009400.
		FT	XX	
		PR	19-JUL-1996;	96FR-00009400.
		PR	XX	
			Location/Qualifiers	
			1. 1698	
			/*tag= a	
			/product= "haemagglutinin protein"	
QY	1 AGCAAAAGCAGGGATATTCTGCAATCATGAAAGACACCATTAATTGTATACTCTGA	60		
Db	1 AGCAAAAGCAGGGATATTCTGCAATCATGAAAGACACCATTAATTGTATACTCTGA	60		
QY	61 CCCATTGGCTCTAGCTAAACCCACAGTGGAAACACAGTGGAAACACATGCTGG	120		
Db	61 CCCATTGGCTCTAGCTAAACCCACAGTGGAAACACAGTGGAAACACATGCTGG	120		
QY	121 GACATCATGCAATGGACATGGTAAACATACTGATACCAATTGGG	180		
Db	121 GACATCATGCAATGGACATGGTAAACATACTGATACCAATTGGG	180		
QY	181 TGACAAATGCTAGTAACTGATGCTAGGATTCATGGAAAAATGCAACACTAT	240		
Db	181 TGACAAATGCTAGTAACTGATGCTAGGATTCATGGAAAAATGCAACACTAT	240		
QY	241 ATAAAGTCTCTAGTGGAAATGGCATTAAATAGTCGAATGCTAGAGCCCCACT	300		
Db	241 ATAGGGTCTCTAGTGGAAATGGCATTAAATAGTCGAATGCTAGAGCCCCACT	300		
QY	301 GTGATGCTCTAGTGGAAATGGCATTAAATAGTCGAATGCTAGAGCCCCACT	360		
Db	301 GTGATGCTCTAGTGGAAATGGCATTAAATAGTCGAATGCTAGAGCCCCACT	360		
QY	361 ATTGTACCCATGACATCCCTGACTATGCTCGGTCATGCTCGGTCATGCTCG	420		
Db	361 ATTGTACCCATGACATCCCTGACTATGCTCGGTCATGCTCGGTCATGCTCG	420		
QY	421 GAACATTAGATTCAAGCAGGGATCACATGGACGGTGTCACTAAACGGAAAGA	480		
Db	421 GAACATTAGATTCAAGCAGGGATCACATGGACGGTGTCACTAAACGGAAAGA	480		

XX	PA (INMR ) RHONE MERIEUX SA.	Db	601 AGCACAACAAATGAGCAGAACAAATTGATGTCAGATTGGCGACTAACAGTC 660
XX	Audonnet JCF, Bouchardon A, Riviere MEA;	Qy	690 ACAAAAGAGTCACAACGATGTCCTTAATCGATCTGACCGTGGTTAGGGT 749
PI		Db	661 ACAAAAGAGTCACAACAAATTATCCCAACTCGATCTGAGCGGGTGGGT 720
XX	WPI: 1998-112826/11.	Qy	750 CAATGGGGATAAGGATAAGGATACTGGACATGTAACCTGGAGATATCGTATGATA 809
DR		Db	721 CAATGGGGATAAGGATAAGGATACTGGACATGTAACCTGGAGATATCGTATGATA 780
DR-PSDB	P-PSDB; AAW44346.	Qy	
XX	Multi-valent polynucleotide vaccines against equine pathogens - consist of at least 3 plasmids able to express protective antigens from specified viruses.	Db	
PT		Qy	810 AACGTAATGGCACTTACTGGACCCGGGATATTAAATTGAAACAGGGAAAGC 869
PT	Example 14; Fig 8; 49pp; French.	Db	781 AACGTAATGGCACTTACTGGACCCGGGATATTCAATGGAAAGCAGGAAAGC 840
PS		Db	
XX	The invention relates to a multivalent vaccine for protecting horses	Qy	870 TCGTAATGAGATACTGGACATTTGCTGATGATTACCCAAAT 929
CC	CC against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially selected from equine herpesvirus (EHV), equine influenza virus (EIV), Clostridium tetani, <i>Borrelia burgdorferi</i> , Eastern, Western or Venezuelan equine encephalomyelitis viruses (EEEV, WEEV and VEEV, respectively) and rabies virus. The vaccines are preferably composed of polynucleotide sequences encoding 3 antigens, all as part of vectors. This sequence represents the coding region of the EIV Fontainebleau strain haemagglutinin gene. The sequence was subcloned into the plasmid pYR1012 to generate plasmid pAB099 for use in the vaccine	Db	841 TCGTAATGAGATACTGGACATTTGCTGATGATTACCCAAAT 900
CC		Qy	930 GGAGCATCCCAAGCAAAACATTCAAAATGAAACAAAGTACATGGAAATG 989
CC		Db	901 GGAGCATCCCAAGCAAAACATTCAAAATGAAACAAAGTACATGGAAATG 960
CC		Qy	990 CCCAGTATATGAGCAAAACATTAAAGCTGCCACTGGATGAGGAATATGGAAATG 1049
CC		Db	961 CCCAGTATATGAGCAAAACATTAAAGCTGCCACTGGATGAGGAATATGGAAATG 1020
CC		Qy	
SQ	Sequence 1698 BP; 604 A; 319 C; 384 G; 391 T; 0 U; 0 Other;	Db	
	Query Match 89.3%; Score 947.2%; DB 2; Length 1698;	Qy	1050 AAGGAAATGAGA 1061
	Best Local Similarity 94.9%; Pred. No. 4.2e-257;	Db	1021 AAGGAAATCAGA 1032
	Matches 979; Conservative 0; Mismatches 53; Indels 0; Gaps 0;	Db	
Qy			
30	ATGAAACAAACCAATTATTGATACTACTGACCCATTGGCTPACAGTCAAACCAACC 89	RESULT 1.2	
1	ATGAAACACCAATTATTGATACTACTGACCCATTGGCTPACAGTCAAACCAACC 60	AAQ72855	
Db		ID AAQ72855 standard; cDNA; 1777 BP	
Qy		XX	
90	AGTGGAAACACACGACATTATGCTGGACACCAGTAGCAATTGGAAATG 149	AC	
61	AGTGCACAAACACACGACACACTATGCTGGACACCAGTAGCAATTGGAAATG 120	XX	
Db		DT 25-MAR-2003 (revised)	
Qy		DT 23-JUN-1995 (first entry)	
150	GTAAAAACAATACTGAGCAAAATTGAGCTGAAATGCTAGATGGAGAAATTGCA 209	XX	
121	GTAAAAACAACTAACTGAGCAAAATTGAGCTGAAATGCTAGATGGAGCA 180	DE	Full length H3N2 influenza A virus, strain A2/Aichi/2/68 HA gene.
Db		XX	
Qy		XX	Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2; PCR; subtype; human; influenza A virus; immunogenic; artificial peptide; antigen; vaccine; infection; polymerase chain reaction; primer; amplify; C119; region A; region B; ds.
210	ATTGATATAGGAAATATGCAACACTCATATAAAAGTCTAGATGGAGAAATTGCA 269	XX	
181	ACTTAAATAGGAAATATGCAACCCATATGGGTTCTAGATGGAGAAACTGCA 240	XX	
Db		XX	
Qy		OS	Influenza A virus.
270	TTAATGATGCAATGCTAGAGACCCACACTGATGCTTCCTCGTAGAAATTGGAC 329	XX	
241	TTAATGATGCAATGCTAGAGACCCACACTGATGCTTCCTCGTAGAAATTGGAC 300	PH	
Db		FT Key	
Qy		FT CDS	36..1737
330	CTCTCTATAGAAAGAGCAGCGTTAGAATGCTACCATATGAAATTACAGAGGGATC 389	FT	/*tag= C
Db		FT	/product= "Full length HA from H3N2 subtype"
301	CTCTCTATAGAAAGAGCAGCGTTAGAATGCTACCATATGAAATTACAGAGGGATC 360	FT	sig_peptide
Db		FT	37..84
Qy		FT	/*tag= d
390	GCATCGCTCCGGTCAATTGATGACATCCTCGAGAACATCTAGAAATTACAGCAGGGATC 449	FT	/product= "Globular head domain"
Db		FT	misc_feature
361	GCATCGCTCCGGTCAATTGATGACATCCTCGAGAACATCTAGAAATTACAGCAGGGATC 420	FT	85..146
Db		FT	/*tag= b
Qy		FT	/product= "Stem region of N-terminal domain"
450	ACATGACAGCTGTCACTCAAAACGGAAGAGTGGCTGCAAAAGGGATAGCCAT 509	FT	247..903
Db		FT	misc_feature
421	ACATGACAGCTGTCACTCAAAACGGAAGAGTGGCTGCAAAAGGGATAGCCAT 480	FT	904..1734
Db		FT	/*tag= e
Qy		FT	/product= "Stem region of C-terminal domain"
510	AGTTCCTTAAGGAGAAACTATACATCTGGTAACAAATTGAAACTCTACCCACAT 569	FT	26-OCT-1994.
481	AGTTCCTTAAGGAGAAACTATACATCTGGTAACAAATTGAAACTCTACCCACAT 540	FT	XX
Db		FT	94BP-003-02819.
Qy		PR	20-APR-1994;
570	GTGACAATGCTAAACATAAAAATTGAGAAACTATACATCTGGGATTCTACACCG 629	PR	20-APR-1993.
541	GTAAATGATGCTAAACATACATACATCTGGGATTCTACACCG 600	PR	93JP-00115216.
630	AGTCACAAACAGCAGCACAGAACATTGATCCAAAGAATTGACAGGAAACAGTC 689	PR	







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Qy 238 CATAATAAAGTCTAGATGGAAAGAAATTGACATTAAATAGATGCAATGCTAGGAGACCCCC 297
Db 241 CTCATCAAATCCTTGATGGAAAAAACTGCACATGTACATGCTCTATGGGACCCCTC 300
Qy 298 ACTGTGATGCTCTCCAGTATGAGAATTGGACCTCTTACATGAAAGAAGAGCGCTTCA 357
Db 301 ATTGTGATGGCTTCAAAATGAAATGGACCTTGTGAAAGCAGAAAGCTTCA 360
Qy 358 GCAATTGCTACCCATATGACATCCCTGACTATGCACTGCTCGTCCATTGTCATCT 417
Db 361 GCAACTGTTACCTTATGATGTCAGATTGCTCTTAGGTCACTGTGCTCGT 420
Qy 418 CAGGAACATTAGAAATTACACGGAGGGATICAATGACAGGGTCACTCAAACCGAA 477
Db 421 CAGGCACCCCTGAGTTATGAGGCTCAATTGACTGCTGGGTCATCGAGATGGG 480
Qy 478 GAAAGTGGAGGCTGCAAAGGGATCAGCCGATAGTTAGCTTTAGGCCAGCTGAATTGGCTAA 537
Db 481 GAAAGTGTGCTGCAAAGGGACCTGATAACAGTTCTCAGTAGACTGCAACTGGTGT 540
Qy 538 CAAAATCTGGAAAACCTTACCCACATGAAATGGCAATGCCTAACAAATAATTTCG 597
Db 541 ACAAAATGAGAACATATTCAAGTGTGAACTGACTAGCCAAACAAAGCACATTGTG 600
Qy 598 ACAAAACTATACATCTGGGATTCTACCGCGAGCTCAACCAACAGCAGACAGATTGT 657
Db 601 ACAAAACTGTACATTGGGACTTCACCCGGGAAAGAACAAACATT 660
Qy 658 ACATCCAGAAGTCAAGGAGTAAAGCTCAACAAAGGAAACAAACGATAATGTC 717
Db 661 ATGTTCAAGCTCAGGGAGTCTACAGTCACCTCCACCAAGGAAAGCCGAAACTATAATCC 720
Qy 718 CTAATATGGATCTAGACCGTGGTTAGGGTCAATCAGGAGGATAAGCATATCTGG 777
Db 721 CGAAATGGCTCTAGACCCCTGGTAAGGGTCTGTCTAGTAGATAAGATCTATTGSA 780
Qy 778 CCATTGTAACACCTGGAGATCTCTAAATGATAAACAGTAATGGCAACTTAGTTGCACCGC 837
Db 781 CAATAGTAAACCGGGAGACATCTGTTAAATGACAGGGAAACTPCTC 840
Qy 838 GGGGATTTTAATGAAACAGGAAAGCTCTGTAAATGAGATCAGTCAACCCATAG 897
Db 841 GGGGTTACTCIAAAATGCACTGGAAAGCTCAATATGAGGTCAATGTCACCTTC 900
Qy 898 ACATTGGTGTCTGAAATGTATTACACAAATGGAAAGCATCCCCAACGACAAACCTTC 957
Db 901 GCACCTGCACTGTCAGTCACTCIAATGAAAGCATCCAAATGCAAGCCTTC 960
Qy 958 AAAATGAAACAAATTAATGAAATGGAAAGCTATATGAGGAAACACTTAA 1017
Db 961 AAAACCTAAACAGATCACATGGGGCATGCCAAATGATGTAAGGAAACACTCTGA 1020
Qy 1018 AGCTGGCACTGGATGGGAAATACAGAAAAGCAATTCTGA 1061
Db 1021 AGTTGGCAACAGGGATGGGAAATGTAACAGGAAACAAACTCTGA 1064

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pBluescript KS(+) after bulk excision from Lambda FLC I.										
TITLE	pBluescript KS(+) after bulk excision from Lambda FLC I.									
	ORIGIN	FEATURES	FEATURES	FEATURES	FEATURES	FEATURES	FEATURES	FEATURES	FEATURES	
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanae,Y., Wells,C., Willmung,L.G., Wyndshaw-Boris,A., Yang,J., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,N., Imotani,K., Iwasa,K., Hayashizume,N., Hirono,N., Hirono-Kishikawa,T., Kawai,J., Aizawa,K., Sakazume,N., Saito,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Iwasa,K., Itoh,M., Kaga,Y., Miyazaki,A., Sakai,K., Sasaki,D., Shibusawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	Query Match Score 4.0%; Best Local Similarity 50.0%; Matches 105; Conservative 0; Mismatches 105; Indels 0; Gaps 0;	
JOURNAL	PUBLISHED	COMMENT	RESULT 8	CNS001RE/C	CNS001RE	1106 bp	DNA linear	GSS 14-JUN-1999		
12466851	2002	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-53-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a>	LOCUS	Drosophila melanogaster genome survey sequence T7 end of BAC: BAC48P05 of RPCI-38 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	DEFINITION					
		Adachi,J., Aizawa,K., Akinura,N., Arakawa,T., Carminci,P., Fukuda,S., Hashizume,W., Hayashizaki,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kaga,Y., Kawai,J., Koijima,Y., Kondo,S., Kono,H., Koya,S., Miyazaki,A., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohnato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibusawa,A., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watanuki,A., Muramatsu,M. and Hayashizaki,Y.	ACCESSION	AL078654	GI:5101944					
		Direct Submission	VERSION	AL078654.1						
		Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)	KEYWORDS	GSS.	Drosophila melanogaster (fruit fly)					
		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)	ORGANISM	Drosophila melanogaster	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.					
		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 capillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)	REFERENCE	Genoscope.	Genoscope. Direct Submission					
		Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)	AUTHORS	Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY Cedex - FRANCE (E-mail : <a href="mailto:sequre@genoscope.cns.fr">sequre@genoscope.cns.fr</a>	JOURNAL					
		Normalizaton and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)	TITLE	- Web : <a href="http://www.genoscope.cns.fr">www.genoscope.cns.fr</a>						
		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 capillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)	COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazuyuki Osoegawa and Aaron Mammober in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y <sup>2</sup> , cn bw sp. The same strain used for the BDGP's P1 and BAC libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <a href="http://bacpac.med.buffalo.edu/drosophila_bac.htm">http://bacpac.med.buffalo.edu/drosophila_bac.htm</a> .						
		Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)	FEATURES	1. 1106	Location/Qualifiers					
		Normalizaton and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)	FEATURES	/organism="Drosophila melanogaster"						
		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 capillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)	FEATURES	/mol_type="genomic DNA"						
		Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)	FEATURES	/db_xref="taxon:7227"						
		Normalizaton and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)	FEATURES	/clone="BACR48P05"						
		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 capillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)	FEATURES	/note="Lib="RPCI-98"						
		Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)	FEATURES	/note="End : T7"						
		Normalizaton and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)	FEATURES							
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AUTHORS	Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Building (1998)							Organism: "Drosophila melanogaster"
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COMMENT	Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 0208 Email: medadam@tigr.org							Organism: "Drosophila melanogaster"
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Indels	0							Organism: "Drosophila melanogaster"
Gaps	0							Organism: "Drosophila melanogaster"
Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tbdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.								Organism: "Drosophila melanogaster"
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Query	199 TAGTCAGACGATTTCATAGGAAACAAACTATCACAAACACAA 258							Organism: "Drosophila melanogaster"





collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CGES) initiative (<http://cggs.stanford.edu>). The clone was isolated from the BAC library CHORI-213 built by Pierie de Jong in collaboration with the Stanford Genome Evolution Center (<http://www.chori.org/bacpac/>). Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).

## ORIGIN

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## RESULT 15

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## ACCESSION

## KEYWORDS

## SOURCE

## ORGANISM

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## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## QUALIFIERS

## ORIGIN

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